MIGRATING MOLECULES – GENETIC IDENTITY AND DIFFERENCE AMONG HUMPBACK WHALES, WORLD-WIDE. *(ABSTRACT)* Over the last decade, molecular genetic investigations of skin biopsy samples collected from humpback whales (*Megaptera novaeangliae*) have provided a remarkable description of the social relationships, migratory habits and historical demography of this cosmopolitan species. In many cases, genetic markers have been used to test and extend previous hypotheses based on long-term studies of naturally marked individuals. In other cases, they have provided novel insights into the evolutionary dynamics and history of populations. Here I first review basic characteristics of the markers used for these studies, including sequence variation in mitochondrial (mt) DNA control region, length differences in alleles of nuclear microsatellite loci (or Short Tandem Repeats), and sequence variation of introns and exons of functional nuclear genes. I then review or introduce selected examples of the applications of these marking from published or ongoing studies in my laboratory, some of which will be presented in greater detail by others at *Humpback Whale Conference 2000*. These include: the identification of individuals in populations; analysis of kinship among social groups; descriptions of maternally directed fidelity to migratory destinations; evidence for sex-biased gene flow between wintering grounds; estimation of long-term gene flow among oceans; and detecting humpback whale products for sale on commercial markets in Japan and Korea.

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WORLD-WIDE DISTRIBUTION OF NUCLEAR GENETIC MARKERS IN HUMPBACK WHALES. *(ABSTRACT)* We compare allelic variation in a nuclear actin intron with that observed in three microsatellite loci among oceanic populations of humpback whales (*Megaptera novaeangliae*). The presence of two highly divergent actin allele lineages was confirmed in the three oceanic populations (Palumbi & Baker, 1994). The distribution of the two lineages is consistent with divergence of each through historic isolation and the subsequent dispersion of both lineages during one or more periods of trans-oceanic gene flow. Sequencing and SSCP analysis resolved the two divergent lineages further into eight alleles. Of the four common alleles, two were globally distributed, one was common only to North Pacific and Southern Indo-Pacific populations, and one was unique to the North Atlantic. Of the rare alleles, southern Indo-Pacific populations shared one, one occurred in a subset of North Pacific and southern Indo-Pacific populations, and two were population specific. In comparison to the intron data, the microsatellite loci showed reduced levels of population differentiation and the absence of unique oceanic alleles, perhaps as a result of size homoplasy. In contrast to the distribution of mtDNA lineages, which suggest a more recent connection between the North Atlantic and southern Indo-Pacific oceans, the distribution of nuclear alleles suggests a more recent historic connection, or male-mediated gene flow, between the southern Indo-Pacific and North Pacific oceans.

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